

4-32761A_UNZ.ST25.txt
SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

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<213> Rattus norvegicus

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<221> PEPTIDE

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Glu Ala

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<213> Mus musculus

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<222> (1)..(221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

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Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
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<223> Light Chain of 11C7 with leader sequence

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Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
 35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
 50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
 65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
 100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 130 135 140

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Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
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<223> Human NogoA

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Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
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gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc 192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
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gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac 240
Page 4

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gct Ala	ccc Pro	ccc Pro	gtc Val 100	gcc Ala	ccg Pro	gag Glu	cgg Arg	cag Gln 105	ccg Pro	tct Ser	tgg Trp	gac Asp 110	ccg Pro	agc Ser	ccg Pro	336
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agt Ser 305	gtc Val	tct Ser	cca Pro	aaa Lys	gca Ala 310	gaa Glu	tct Ser	gcc Ala	gta Val	ata Ile 315	gta Val	gca Ala	aat Asn	cct Pro	agg Arg 320	960

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cct Pro	ttg Leu	tta Leu	gga Gly	gat Asp 485	cct Pro	act Thr	tca Ser	gaa Glu	aat Asn 490	aag Lys	acc Thr	gat Asp	gaa Glu	aaa Lys 495	aaa Lys	1488
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Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser 635 tca tca cca tta gaa	
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gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg	2496
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1190															
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35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

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180 185 190

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195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

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225 230 235 240

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245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
260 265 270

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275 280 285

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290 295 300

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Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
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405 410 415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
420 425 430

Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
435 440 445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
450 455 460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
465 470 475 480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
485 490 495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
500 505 510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp
515 520 525

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Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
 530 535 540
 Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
 545 550 555 560
 Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
 565 570 575
 Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
 580 585 590
 Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
 595 600 605
 Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
 610 615 620
 Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
 625 630 635 640
 Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
 645 650 655
 Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
 660 665 670
 Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
 675 680 685
 Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
 690 695 700
 Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
 705 710 715 720
 Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
 725 730 735
 Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
 740 745 750
 Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
 755 760 765
 Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
 770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu
995 1000 1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala
1010 1015 1020

Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
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1025

1030

1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
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Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
 1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
 1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
 1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
 1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
 1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
 1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
 1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
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Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
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Glu Ala

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<211> 819

<212> PRT

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<220>

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<222> (1)..(819)

<223> human Nig

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 35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
 50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
 65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
 85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
 100 105 110

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Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val
305 310 315 320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
355 360 365

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Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
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 Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
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 405 410 415
 Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
 420 425 430
 Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
 435 440 445
 Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
 450 455 460
 Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
 465 470 475 480
 Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
 485 490 495
 Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
 500 505 510
 Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
 515 520 525
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 Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
 545 550 555 560
 Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
 565 570 575
 Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
 580 585 590
 Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
 595 600 605
 Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
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610

615

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
805 810 815

Lys Thr Ser

<210> 8

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<223> hypervariable part of heavy chain of 11C7

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Asp

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<211> 30

<212> DNA

<213> Mus musculus

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<212> DNA

<213> Mus musculus

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<221> misc_binding

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<223> DNA-CDR2-11C7

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<211> 27

<212> DNA

<213> Mus musculus

<220>

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<222> (1)..(27)

<223> DNA-CDR3-11C7

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<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(48)

<223> DNA-CDR'1-11C7

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<212> DNA

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<221> misc_binding

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<223> DNA-CDR'2-11C7

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21

<210> 19

<211> 27

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<220>

<221> misc_binding

<222> (1)..(27)

<223> DNA-CDR'3-11C7

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27

<210> 20

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<212> DNA

<213> Mus musculus

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<222> (1)..(54)

<223> leader sequence for heavy chain of 11C7

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cag tgt 54
 Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

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Gln Cys

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<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(57)

<223> leader sequence for 11C7-light chain

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 1 5 10 15

acc agc ggt 57
 Thr Ser Gly

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<211> 19

<212> PRT

<213> Mus musculus

<400> 23

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Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> Homo sapiens

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<221> PEPTIDE

<222> (1)..(181)

<223> human Nig-D20

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 20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
 50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
 65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
 85 90 95

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Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
115 120 125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
130 135 140

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145 150 155 160

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165 170 175

Pro Val Asp Leu Phe
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<210> 25

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<212> DNA

<213> Rattus norvegicus

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<221> CDS

<222> (1)..(3492)

<223> rat NogoA

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ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc 96
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
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Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192
Glu Asp Leu Glu Glu Leu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac 240
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Leu 65	Ser	Ala	Ala	Ala	Val 70	Pro	Pro	Ala	Ala	Ala 75	Ala	Pro	Leu	Leu	Asp 80	
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Phe	Ser	Ser	Asp	Ser 85	Val	Pro	Pro	Ala	Pro 90	Arg	Gly	Pro	Leu	Pro 95	Ala	
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Ala	Pro	Pro	Ala 100	Ala	Pro	Glu	Arg	Gln 105	Pro	Ser	Trp	Glu	Arg 110	Ser	Pro	
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Ala	Ala	Pro 115	Ala	Pro	Ser	Leu	Pro 120	Pro	Ala	Ala	Ala	Val 125	Leu	Pro	Ser	
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Lys	Leu 130	Pro	Glu	Asp	Asp	Glu 135	Pro	Pro	Ala	Arg	Pro 140	Pro	Pro	Pro	Pro	
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Phe	Ala	Leu	Pro 180	Ala	Ala	Ser	Glu	Pro 185	Val	Ile	Pro	Ser	Ser 190	Ala	Glu	
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Gln	Glu	Asp	Phe	Pro	Ser	Val 215	Leu	Leu	Glu	Thr	Ala 220	Ala	Ser	Leu	Pro	
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Val	Asn	Arg 275	Asp	Leu	Ala	Glu	Phe 280	Ser	Glu	Leu	Glu	Tyr 285	Ser	Glu	Met	
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Gly	Ser 290	Ser	Phe	Lys	Gly	Ser 295	Pro	Lys	Gly	Glu	Ser 300	Ala	Ile	Leu	Val	
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu 310	Val	Ile	Val	Arg	Ser 315	Lys	Asp	Lys	Glu	Asp 320	

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Lys Glu Asp Arg 340 Val Val Ser Pro Glu 345 Lys Thr Met Asp Ile 350 Phe Asn	
gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac	1104
Glu Met 355 Gln Met Ser Val Val Ala 360 Pro Val Arg Glu 365 Tyr Ala Asp	
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Ser Arg Asp Val Leu 390 Ala Ala Arg Ala Asn Val 395 Glu Ser Lys Val Asp 400	
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Arg Lys Cys Leu Glu 405 Asp Ser Leu Glu Gln 410 Lys Ser Leu Gly Lys 415 Asp	
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Ser Glu Gly Arg 420 Asn Glu Asp Ala Ser 425 Phe Pro Ser Thr Pro 430 Glu Pro	
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Gln Ile Ile Thr Glu 485 Lys Thr Ser Pro Lys 490 Thr Ser Asn Pro Phe 495 Leu	
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tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro 675 680 685	2064
agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser 690 695 700	2112
gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu 705 710 715 720	2160
cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr 725 730 735	2208
caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser 740 745 750	2256
gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln 755 760 765	2304
gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser 770 775 780	2352
aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu 785 790 795 800	2400
aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn 805 810 815	2448
gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr 815 820 825	2496

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825 830

820	ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt	2544
	Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe	
	835 840 845	
	gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat	2592
	Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp	
	850 855 860	
	cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca	2640
	Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala	
	865 870 875 880	
	gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat	2688
	Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn	
	885 890 895	
	ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat	2736
	Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn	
	900 905 910	
	agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct	2784
	Arg Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala	
	915 920 925	
	ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt	2832
	Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu	
	930 935 940	
	acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac	2880
	Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp	
	945 950 955 960	
	aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt	2928
	Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val	
	965 970 975	
	gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt	2976
	Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe	
	980 985 990	
	ggg gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc	3024
	Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val	
	995 1000 1005	
	agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc	3069
	Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile	
	1010 1015 1020	
	agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca	3114
	Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	
	1025 1030 1035	
	gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	3159
	Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	
	1040 1045 1050	
	ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt	3204
	Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly	
	1055 1060 1065	
	cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt	3249

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His Val	Asn Ser Thr Ile	Lys	Glu Leu Arg Arg	Leu	Phe Leu Val	
1070		1075		1080		
gat gat	tta gtt gat tcc	ctg	aag ttt gca gtg	ttg	atg tgg gtg	3294
Asp Asp	Leu Val Asp Ser	Leu	Lys Phe Ala Val	Leu	Met Trp Val	
1085		1090		1095		
ttt act	tat gtt ggt gcc	ttg	ttc aat ggt ctg	aca	cta ctg att	3339
Phe Thr	Tyr Val Gly Ala	Leu	Phe Asn Gly Leu	Thr	Leu Leu Ile	
1100		1105		1110		
tta gct	ctg atc tca ctc	ttc	agt att cct gtt	att	tat gaa cgg	3384
Leu Ala	Leu Ile Ser Leu	Phe	Ser Ile Pro Val	Ile	Tyr Glu Arg	
1115		1120		1125		
cat cag	gtg cag ata gat	cat	tat cta gga ctt	gca	aac aag agt	3429
His Gln	Val Gln Ile Asp	His	Tyr Leu Gly Leu	Ala	Asn Lys Ser	
1130		1135		1140		
gtt aag	gat gcc atg gcc	aaa	atc caa gca aaa	atc	cct gga ttg	3474
Val Lys	Asp Ala Met Ala	Lys	Ile Gln Ala Lys	Ile	Pro Gly Leu	
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aag cgc	aaa gca gat tga					3492
Lys Arg	Lys Ala Asp					
1160						

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<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Glu Asp Ile	Asp Gln Ser Ser	Leu Val	Ser Ser Ser Thr	Asp Ser	
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Pro Pro Arg	Pro Pro Pro Ala	Phe Lys Tyr Gln	Phe Val Thr	Glu Pro	
	20	25	30		
Glu Asp Glu	Glu Asp Glu Glu	Glu Glu Glu Asp	Glu Glu Glu Asp	Asp	
	35	40	45		
Glu Asp Leu	Glu Glu Leu	Glu Val Leu Glu Arg	Lys Pro Ala Ala	Gly	
	50	55	60		
Leu Ser Ala Ala	Ala Val Pro Pro	Ala Ala Ala	Ala Pro Leu Leu	Asp	
65	70	75		80	
Phe Ser Ser Asp	Ser Val Pro Pro	Ala Pro Arg Gly	Pro Leu Pro	Ala	
	85	90	95		

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Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

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Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
 355 360 365
 Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
 370 375 380
 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
 385 390 395 400
 Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
 405 410 415
 Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
 420 425 430
 Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
 435 440 445
 Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
 450 455 460
 Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
 465 470 475 480
 Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
 485 490 495
 Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
 500 505 510
 Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
 515 520 525
 Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
 530 535 540
 Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
 545 550 555 560
 Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
 565 570 575
 Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 580 585 590
 Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
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595

600

605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
 610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
 625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
 645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
 660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
 675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
 690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
 705 710 715 720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
 725 730 735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
 740 745 750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
 755 760 765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
 770 775 780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
 785 790 795 800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
 805 810 815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
 820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
 835 840 845

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Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
 850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
 865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
 885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
 900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
 915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
 930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
 945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
 965 970 975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
 1085 1090 1095

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Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

<210> 27

<211> 25

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> rat PEP4

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Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer_bind

<222> (1)..(28)

<223>

<400> 30
aactgcagta ctgagctcct ccatctgc

28

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'

<220>

<221> primer_bind

<222> (1)..(33)

<223> forward primer

<400> 31
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33

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> reverse 5'

<220>

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<223> reverse primer

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gttctcgcagt tatgaagttt tactcag

27

<210> 33

<211> 29

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<223> forward 5'-1

<220>

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<222> (1)..(29)

<223> primer

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29

<210> 34

<211> 28

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<223> reverse 5'-1

<220>

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28

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 <223> primer

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20

<210> 36
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 <212> DNA
 <213> Artificial Sequence

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 <223> 5' primer 2
 <220>
 <221> primer_bind
 <222> (1)..(22)
 <223> primer

<400> 36
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22

<210> 37
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

<400> 37
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24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer_bind

<222> (1)..(22)

<223> primer

<400> 38
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22

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VL leader

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 39

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28

<210> 40

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> 3'-Ck

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<221> primer_bind

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<211> 31

<212> DNA

<213> Artificial Sequence

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<223> 5'-VH leader

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<221> primer_bind

<222> (1)..(31)

<223> primer

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31

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> 3'-CH hinge

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

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24

<210> 43

<211> 663

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(663)

<223> DNA variable part of heavy chain 11C7

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aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120
gtagtctcag gattcgattt tagaagaaat tggatgagtt ggggccggca ggctcctggg 180

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gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg	360
tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca	420
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ctgggatgcc tgggtcaagg ctattttccct gagccagtga cagtgcactg gaactctgga	540
tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgacct ctacactctg	600
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gcc	663

<210> 44

<211> 717

<212> DNA

<213> Mus musculus

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<221> misc_binding

<222> (1)..(717)

<223> variable part of light chain of 11c7

<400> 44

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tcttgcaagt caagtcagag cctcttgcag agtgatggaa agacatattt gaattgggtg	180
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ggagtccctg acagggttcac tggcagtggga tcaggggacgg atttcacact gaaaatcagc	300
agagtggagg ctgaggattt gggactttat tattgctggc aaggtaacac ttttcctcag	360
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc	420
atcttccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg	480
aacaacttct accccaaaga catcaatgtc aagtgggaaga ttgatggcag tgaacgacaa	540
aatggcggtc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc	600
agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc	660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag	717

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